

WHAT IS CLAIMED IS:

1. A method for determining the likelihood of tumor re-occurrence in a patient previously diagnosed with a breast tumor, said method comprising:
  - (1) providing a target cell sample from said patient, wherein said target cell sample comprises morphologically normal breast cells associated with the tumor;
  - (2) analyzing the target cell sample for loss of heterozygosity (LOH) at chromosomal locus 3p24.3; and
  - (3) classifying samples having LOH at chromosomal locus 3p24.3 as positive, wherein a positive sample indicates a greater likelihood of tumor re-occurrence.
2. The method of claim 1, wherein the breast tumor cells have previously been determined to have LOH at 3p24.3.
3. The method of claim 1, wherein said patient has undergone a surgical procedure to treat said previously diagnosed breast tumor.
4. A method of determining post-surgical treatment for a breast cancer patient, said method comprising:
  - (1) providing a target cell sample from said patient, wherein said target cell sample comprises morphologically normal breast cells associated with the breast cancer cells;
  - (2) analyzing the target cell sample for loss of heterozygosity (LOH) at chromosomal locus 3p24.3; and

- (3) classifying samples having LOH at chromosomal locus 3p24.3 as positive, wherein a positive sample is an indicator that more aggressive post-surgical treatment is required.
5. The method of claim 4, wherein the breast cancer cells have previously been determined to have LOH at 3p24.3.
6. A method of identifying a patient as being at risk for breast cancer, said method comprising:
  - (1) obtaining a breast tissue cell sample from said patient;
  - (2) analyzing the breast tissue cell sample for loss of heterozygosity (LOH) at chromosomal locus 3p24.3; and
  - (3) classifying patients whose breast tissue cell sample exhibit LOH at chromosomal locus 3p24.3 as at risk of breast cancer.
7. The method of Claim 6, wherein said breast tissue cell sample is selected from the group consisting of nipple aspirate fluid, ductal lavage fluid, and breast tissue biopsy tissue.
8. A method for determining the likelihood of tumor re-occurrence in a patient previously diagnosed with a breast tumor, said method comprising:
  - (1) providing a target cell sample from said patient, wherein said target cell sample comprises morphologically normal cells from tissue peripheral to the carcinoma cells;
  - (2) analyzing the target cell sample for the level of expression of thyroid hormone receptor  $\beta 1$  compared to a control cell sample; and

- (3) classifying a target cell sample having a lower level of expression of thyroid hormone receptor  $\beta 1$  compared to the control cell sample as positive, wherein a positive sample indicates a greater likelihood of tumor re-occurrence.
9. The method of Claim 8, wherein the level of expression of thyroid hormone receptor  $\beta 1$  is determined by analyzing the amount of mRNA for thyroid hormone receptor  $\beta 1$ .
10. The method of Claim 8, wherein the level of expression of thyroid hormone receptor  $\beta 1$  is determined by analyzing the amount of thyroid hormone receptor  $\beta 1$  protein.
11. A method of determining post-surgical treatment for a breast cancer patient, said method comprising:
  - (1) providing a target cell sample from said patient, wherein said target cell sample comprises morphologically normal cells from tissue peripheral to the carcinoma cells;
  - (2) analyzing the target cell sample for the level of expression of thyroid hormone receptor  $\beta 1$  compared to a control cell sample;
  - (3) classifying a target cell sample having a lower level of expression of thyroid hormone receptor  $\beta 1$  compared to a control cell sample as positive, wherein a positive sample is an indicator that more aggressive post-surgical treatment is required.

12. The method of Claim 11, wherein the level of expression of thyroid hormone receptor  $\beta 1$  is determined by analyzing the amount of mRNA for thyroid hormone receptor  $\beta 1$ .
13. The method of Claim 11, wherein the level of expression of thyroid hormone receptor  $\beta 1$  is determined by analyzing the amount of thyroid hormone receptor  $\beta 1$  protein.
14. A method of identifying a patient as at risk for breast cancer, said method comprising:
  - (1) obtaining a breast tissue cell sample from said patient;
  - (2) analyzing the breast tissue cell sample for the level of expression of thyroid hormone receptor  $\beta 1$  compared to a control cell sample; and
  - (3) classifying a patient whose breast tissue cell samples have a lower level of expression of thyroid hormone receptor  $\beta 1$  compared to a control cell sample as at risk for breast cancer.
15. The method of Claim 14, wherein said breast tissue cell sample is selected from the group consisting of nipple aspirate fluid, ductal lavage fluid, and breast tissue biopsy tissue.
16. The method of Claim 14, wherein the level of expression of thyroid hormone receptor  $\beta 1$  is determined by analyzing the amount of mRNA for thyroid hormone receptor  $\beta 1$ .
17. The method of Claim 14, wherein the level of expression of thyroid hormone receptor  $\beta 1$  is determined by analyzing the amount of thyroid hormone receptor  $\beta 1$  protein.

18. A method of screening for a test compound useful for treatment of breast cancer comprising:
- (1) providing cells from a breast cancer cell line having a hypermethylated promoter at the thyroid hormone receptor  $\beta 1$  gene;
  - (2) contacting said cells with said test compound;
  - (3) determining the level of thyroid hormone receptor  $\beta 1$  expression in said cells in the absence and the presence of said test compound; and
  - (4) selecting a test compound producing an increase in the level of expression of thyroid hormone receptor  $\beta 1$  in the presence of the test compound.
19. The method of claim 18, wherein the breast cancer cell line is selected from the group comprising MDA435, SKBR3 and DU4475.
20. The method of claim 18, wherein the level of thyroid hormone receptor  $\beta 1$  expression is determined by analyzing the amount of mRNA for thyroid hormone receptor  $\beta 1$ .
21. The method of claim 18, wherein the level of thyroid hormone receptor  $\beta 1$  expression is determined by analyzing the amount of thyroid hormone receptor  $\beta 1$  protein.
22. The method of claim 18, wherein the level of thyroid hormone receptor  $\beta 1$  expression is determined by analyzing the methylation level of the thyroid hormone receptor  $\beta 1$  gene promoter.